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<110> Ono Pharmaceutical Co., Ltd.

<120> A novel polypeptide, a cDNA encoding the polypeptide
and utilization thereof

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<150> PCT/JP99/02284

<151> 1999-04-28

<150> JP HEI 10-119731

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<170> PatentIn Ver. 2.1

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 embryonic heart

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embryonic heart

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cag atg gat gaa ggc aac cag tgt gtg gat gtg gac gag tgt gca aca	669
Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr	
95 100 105 110	
 gac tca cac cag tgc aac cct acc cag atc tgt atc aac act gaa gga	717
Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly	
115 120 125	
 ggg tac acc tgc tcc tgc acc gat ggg tac tgg ctt ctg gaa ggg cag	765
Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln	
130 135 140	
 tgc cta gat att gat gaa tgt cgc tat ggt tac tgc cag cag ctc tgt	813
Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys	
145 150 155	
 gca aat gtt cca gga tcc tat tcc tgt aca tgc aac cct ggt ttc acc	861
Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr	
160 165 170	
 ctc aac gac gat gga agg tct tgc caa gat gtg aac gag tgc gaa act	909
Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr	
175 180 185 190	
 gag aat ccc tgt gtt cag acc tgt gtc aac acc tat ggc tct ttc atc	957
Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile	
195 200 205	
 tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc	1005
Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys	
210 215 220	
 agt gat atg gac gag tgc agc ttc tcc gag ttc ctc tgt caa cac gag	1053
Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu	
225 230 235	
 tgt gtg aac cag ccg ggc tca tac ttc tgc tcg tgc cct cca ggc tac	1101
Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr	
240 245 250	
 gtc ctg ttg gat gat aac cga agc tgc cag gat atc aat gaa tgt gag	1149
Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu	
255 260 265 270	
 cac cga aac cac acg tgt acc tca ctg cag act tgc tac aat cta caa	1197
His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln	
275 280 285	

ggg ggc ttc aaa tgt att gat ccc atc agc tgt gag gag cct tat ctg 1245
 Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu
 290 295 300

ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc 1293
 Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys
 305 310 315

aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca 1341
 Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser
 320 325 330

gga cgc tcc gtt cct gct gac atc ttc cag atg caa gca aca acc cga 1389
 Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg
 335 340 345 350

tac cct ggt gcc tat tac att ttc cag atc aaa tct ggc aac gag ggt 1437
 Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly
 355 360 365

cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg 1485
 Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val
 370 375 380

atg aca cgc ccc atc aaa ggg cct cgg gac atc cag ctg gac ttg gag 1533
 Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu
 385 390 395

atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc 1581
 Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile
 400 405 410

cga ctg cgg ata tat gtg tcg cag tat ccg ttc tgagcctctg gctaaggcct 1634
 Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
 415 420 425

ctgacactgc ctttcaccag caccgagggg cgggaggaga aaggaaacca gcaagaatga 1694

gagcgagaca gacattgcac ctttcctgct gaatatctcc tgggggcatc agcctagcat 1754

cttgacccat atctgtacta ttgcagatgg tcaactctgaa ggacaccctg ccctcagttc 1814

ctatgatgca gttatccaaa agtgttcatc ttagcccctg atatgaggtt gccagtgact 1874

cttcaaagcc ttccatttat ttccatcggt ttataaaaaa gaaaatagat tagatttgct 1934

ggggtatgag tcctcgaagg ttcaaaagac tgagtggctt gctctcacct cttcctctcc 1994

ttctccatc tcttgctgca ttgctgcttt gcaaaagtcc tcatgggctc gtgggaaatg 2054
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 tgaagaaaaa aaaaa 2429

<210> 8
 <211> 461
 <212> PRT
 <213> Mus musculus
 <223> Clone mouse A55b derived from Day 13 mouse
 embryonic heart

<400> 8
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 Arg Arg Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His
 -20 -15 -10 -5
 Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg
 -1 1 5 10
 Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
 15 20 25
 Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu
 30 35 40
 Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
 45 50 55 60
 Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val
 65 70 75
 Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe
 80 85 90

Gly	Tyr	Gln	Met	Asp	Glu	Gly	Asn	Gln	Cys	Val	Asp	Val	Asp	Glu	Cys	95	100	105	
Ala	Thr	Asp	Ser	His	Gln	Cys	Asn	Pro	Thr	Gln	Ile	Cys	Ile	Asn	Thr	110	115	120	
Glu	Gly	Gly	Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp	Leu	Leu	Glu	125	130	135	140
Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly	Tyr	Cys	Gln	Gln	145	150	155	
Leu	Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	Ser	Cys	Thr	Cys	Asn	Pro	Gly	160	165	170	
Phe	Thr	Leu	Asn	Asp	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val	Asn	Glu	Cys	175	180	185	
Glu	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr	Tyr	Gly	Ser	190	195	200	
Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu	Asp	Gly	Ile	205	210	215	220
His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu	Phe	Leu	Cys	Gln	225	230	235	
His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Ser	Tyr	Phe	Cys	Ser	Cys	Pro	Pro	240	245	250	
Gly	Tyr	Val	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp	Ile	Asn	Glu	255	260	265	
Cys	Glu	His	Arg	Asn	His	Thr	Cys	Thr	Ser	Leu	Gln	Thr	Cys	Tyr	Asn	270	275	280	
Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Ser	Cys	Glu	Glu	Pro	285	290	295	300
Tyr	Leu	Leu	Ile	Gly	Glu	Asn	Arg	Cys	Met	Cys	Pro	Ala	Glu	His	Thr	305	310	315	
Ser	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp	Met	Asp	Val	320	325	330	
Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	Ile	Phe	Gln	Met	Gln	Ala	Thr	335	340	345	

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
 350 355 360

Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr
 365 370 375 380

Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp
 385 390 395

Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser
 400 405 410

Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
 415 420 425

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<211> 423

<212> PRT

<213> Mus musculus

<400> 9

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Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
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Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
 35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
 50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
 65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
 85 90 95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
 100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
 115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
 130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
 145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
 165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
 180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
 195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp
 210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
 225 230 235 240

Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
 245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
 260 265 270

Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
 275 280 285

Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
 290 295 300

Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
 305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
 325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
 340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
 355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380

Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
 385 390 395 400

Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
 405 410 415

Tyr Val Ser Gln Tyr Pro Phe
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 <211> 1269
 <212> DNA
 <213> Mus musculus

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 tgccggacca tccctgaggc ttgtcgtggg gacatgatgt gtgtcaacca gaatggcggg 120
 tatttgtgca tccctcgaac caaccagtg tatcgagggc cttactcaaa tccctactct 180
 acatcctact caggcccata cccagcagcg gcccaccag taccagcttc caactacccc 240
 acgatttcaa ggctcttgt ctgccgcttt gggatcaga tggatgaagg caaccagtg 300
 gtggatgtgg acgagtgtgc aacagactca caccagtga accctacca gatctgtatc 360
 aacactgaag gaggttacac ctgctcctgc accgatgggt actggcttct ggaagggcag 420
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 caagatgtga acgagtgcga aactgagaat ccctgtgttc agacctgtgt caacacctat 600
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 ctgattgggtg aaaaccgctg tatgtgtcct gctgagcaca ccagctgcag agaccagcca 960
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 ttccagatgc aagcaacaac ccgataccct ggtgcctatt acattttcca gatcaaactc 1080
 ggcaacgagg gtcgagagtt ctatatgcgg caaacagggc ctatcagtgc caccctgggtg 1140
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 aacactgtca tcaacttcag aggcagctcc gtgatccgac tgcggatata tgtgtcgcag 1260
 tatccgttc 1269

<210> 11
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<400> 11
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aaccaaaatg gcgggtatgt atgcattccc cggacaaacc ctgtgtatcg agggccctac 240
tcgaaccctt actcgacccc ctactcaggt ccgtacccag cagctgcccc accactctca 300
gctccaaact atcccacgat ctccaggcct cttatatgcc gctttggata ccagatggat 360
gaaagcaacc aatgtgtgga tgtggacgag tgtgcaacag attcccacca gtgcaacccc 420
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tgcgtcaaca cctacggctc ttcatctgc cgctgtgacc caggatatga acttgaggaa 720
gatggcggtt attgcagtga tatggacgag tgcagcttct ctgagttcct ctgccaacat 780
gagtgtgtga accagcccgg cacatacttc tgctcctgcc ctccaggcta catcctgctg 840
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ttccagatca aatctgggaa tgagggcaga gaattttaca tgcggcaaac gggcccatc 1200
agtgccaccc tggatgatgac acgccccatc aaagggcccc gggaaatcca gctggacttg 1260
gaaatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtgat ccgactgcgg 1320
atatatgtgt cgcagtaccc attc                                     1344

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<210> 12

<211> 2328

<212> DNA

<213> Homo sapiens

<220>

<223> Clone human A55 derived from human brain

<220>

<221> CDS

<222> (169)..(1512)

<220>

<221> sig_peptide

<222> (169)..(237)

<220>

<221> mat_peptide

<222> (238)..(1512)

<400> 12

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ccgcgagccc cgagggccca gaggaggccg acgtgcccga gctcctccgg gggccccgcc 120

cgcgagcttt cttctcgct tgcacatctcc tcctcgcgcg tcttggac atg cca gga 177
 Met Pro Gly

ata aaa agg ata ctc act gtt acc att ctg gct ctc tgt ctt cca agc 225
 Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser
 -20 -15 -10 -5

cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac ctg gat cgc 273
 Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg
 -1 1 5 10

cag tca gga cag tgt tta gat att gat gaa tgc cga acc atc ccc gag 321
 Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
 15 20 25

gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc ggg tat tta 369
 Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu
 30 35 40

tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac tcg aac ccc 417
 Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
 45 50 55 60

tac tcg acc ccc tac tca ggt ccg tac cca gca gct gcc cca cca ctc 465
 Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu
 65 70 75

tca gct cca aac tat ccc acg atc tcc agg cct ctt ata tgc cgc ttt 513
 Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe
 80 85 90

gga tac cag atg gat gaa agc aac caa tgt gtg gat gtg gac gag tgt 561
 Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys
 95 100 105

gca aca gat tcc cac cag tgc aac ccc acc cag atc tgc atc aat act 609
 Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
 110 115 120

gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg ctt ctg gaa 657
 Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu
 125 130 135 140

ggc cag tgc tta gac att gat gaa tgt cgc tat ggt tac tgc cag cag 705
 Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln
 145 150 155

ctc tgt gcg aat gtt cct gga tcc tat tct tgt aca tgc aac cct ggt 753

Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
 160 165 170

ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg aac gag tgt 801
 Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys
 175 180 185

gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct 849
 Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
 190 195 200

ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt 897
 Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val
 205 210 215 220

cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc ctc tgc caa 945
 His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
 225 230 235

cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca 993
 His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro
 240 245 250

ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac atc aac gaa 1041
 Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu
 255 260 265

tgt gag cac agg aac cac acg tgc aac ctg cag cag acg tgc tac aat 1089
 Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn
 270 275 280

tta caa ggg ggc ttc aaa tgc atc gac ccc atc cgc tgt gag gag cct 1137
 Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro
 285 290 295 300

tat ctg agg atc agt gat aac cgc tgt atg tgt cct gct gag aac cct 1185
 Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro
 305 310 315

ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac atg gac gtg 1233
 Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
 320 325 330

gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg caa gcc acg 1281
 Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
 335 340 345

acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa tct ggg aat 1329

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Glu	Gly	Arg	Glu	Phe	Tyr	Met	Arg	Gln	Thr	Gly	Pro	Ile	Ser	Ala	Thr	
365					370					375					380	
ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc cag ctg gac 1425																
Leu	Val	Met	Thr	Arg	Pro	Ile	Lys	Gly	Pro	Arg	Glu	Ile	Gln	Leu	Asp	
			385						390					395		
ttg gaa atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc 1473																
Leu	Glu	Met	Ile	Thr	Val	Asn	Thr	Val	Ile	Asn	Phe	Arg	Gly	Ser	Ser	
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gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc tgagcctcgg 1522																
Val	Ile	Arg	Leu	Arg	Ile	Tyr	Val	Ser	Gln	Tyr	Pro	Phe				
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ccaaactgat taaatatttg aagaga 2328																

<210> 13
 <211> 448
 <212> PRT
 <213> Homo sapiens
 <223> Clone human A55 derived from human brain

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Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
 10 15 20 25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
 30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
 45 50 55

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
 60 65 70

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
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Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
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Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
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Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
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Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
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Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
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Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
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Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
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Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
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 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
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 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
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 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
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 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
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 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
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 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
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 Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
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 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
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 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
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 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
 365 370 375
 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
 380 385 390
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<213> Homo sapiens

<400> 14

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Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser
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Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro
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Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu
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Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
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Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
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Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
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Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
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Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240

Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp
 245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
 260 265 270

Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
 275 280 285

Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp
 290 295 300

Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
 305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
 325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
 340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
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Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380

Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val
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Tyr Val Ser Gln Tyr Pro Phe
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<211> 1269

<212> DNA

<213> Homo sapiens

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<213> Artificial Sequence

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SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel polypeptides, cDNA coding these polypeptides and Use thereof

<130> ONF-2970PCT

<141> 1999-04-28

<150> JP 10-119731

<151> 1998-04-28

<160> 17

<170> PatentIn Ver. 2.0

<210> 1

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<212> PRT

<213> Mus musculus

<400> 1

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-10

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-5

1

5

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 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
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 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
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 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val
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 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val
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 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
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 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
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Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe			
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Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser			
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Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp			
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Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr			
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Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys			
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Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala			
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Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp			
315	320	325	
Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met			
330	335	340	345
Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys			
350	355	360	
Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile			
365	370	375	
Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile			
380	385	390	
Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg			
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<212> DNA

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Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
-20 -15
ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca 158
Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
-10 -5 -1 1 5
aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
10 15 20
gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254
Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
25 30 35
aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
40 45 50
cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350
Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
55 60 65
cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398
Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
70 75 80 85
agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag 446
Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln

90	95	100	
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Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro			
105	110	115	
acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc ac	542		
Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr			
120	125	130	
gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt	590		
Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys			
135	140	145	
cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat	638		
Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr			
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tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct	686		
Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser			
170	175	180	
tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc	734		
Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr			
185	190	195	
tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat	782		
Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr			
200	205	210	
gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc	830		
Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser			
215	220	225	
ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca	878		

Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser
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Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg
 250 255 260
agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc 974
Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr
 265 270 275
tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat 1022
Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp
 280 285 290
ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt 1070
Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys
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atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc 1118
Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile
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ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac 1166
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Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln
 360 365 370

aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg 1310
Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly

375

380

385

cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc 1358
Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val

390

395

400

405

atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tgc 1406
Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser

410

415

420

cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag 1458
Gln Tyr Pro Phe

425

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<212> PRT

<213> Mus musculus

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50 55 60
Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
65 70 75 80
Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95
Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140
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145 150 155 160
 Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
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 Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
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 Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
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 Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp
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 Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
 225 230 235 240
 Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
 245 250 255
 Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
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 275 280 285
 Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
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 Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
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 Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
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 Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
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<212> DNA

<213> Mus musculus

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<212> PRT

<213> Mus musculus

<400> 6

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-20

-15

-10

-5

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-1	1	5	10
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Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu			
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Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro			
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Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val			
65	70	75	
Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe			
80	85	90	
Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys			
95	100	105	
Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr			
110	115	120	
Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu			
125	130	135	140
Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln			
145	150	155	
Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly			
160	165	170	
Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys			
175	180	185	
Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser			
190	195	200	
Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile			

205	210	215	220
His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln			
	225	230	235
His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro			
	240	245	250
Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu			
	255	260	265
Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn			
	270	275	280
Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro			
285	290	295	300
Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr			
	305	310	315
Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val			
	320	325	330
Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr			
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Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn			
	350	355	360
Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr			
365	370	375	380
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp			
	385	390	395
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser			
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420

425

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<211> 1383

<212> DNA

<213> Mus musculus

<400> 7

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<210> 8

<211> 2429

<212> DNA

<213> Mus musculus

<220>

<223> Clone mouse A55b derived from Day 13 mouse embryonic heart

<220>

<221> CDS

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<220>

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<222> (232).. (339)

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<222> (340)..(1614)

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gactgctgac tacggcacca gcaattgctt tgctgcgacg gctgtgagac aagcagaagt 180
ctccgaacac ttctgtctgc gtttgcctta tgtgtgtgat ttacagaggg a atg gga 237

Met Gly

-35

cct aga agt ttc gag cca atg cac agt gga ctc tgc aga cag aga cgc 285
Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln Arg Arg

-30

-25

-20

atg ata ctc act gtt acc atc ttg gca ctc tgg ctt cca cat cct ggg 333
Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His Pro Gly

-15

-10

-5

aat gca cag cag cag tgc aca aac ggc ttt gac ctg gac cgc cag tca 381
Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser

-1 1

5

10

gga cag tgt cta gat att gat gaa tgc cgg acc atc cct gag gct tgt 429
Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys

15

20

25

30

cgt ggg gac atg atg tgt gtc aac cag aat ggc ggg tat ttg tgc atc 477
Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile

35

40

45

cct cga acc aac cca gtg tat cga ggg cct tac tca aat ccc tac tct 525

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Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala	
65 70 75	
tcc aac tac ccc acg att tca agg cct ctt gtc tgc cgc ttt ggg tat	621
Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr	
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Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr	
95 100 105 110	
gac tca cac cag tgc aac cct acc cag atc tgt atc aac act gaa gga	717
Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly	
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Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln	
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Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys	
145 150 155	
gca aat gtt cca gga tcc tat tcc tgt aca tgc aac cct ggt ttc acc	861
Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr	
160 165 170	
ctc aac gac gat gga agg tct tgc caa gat gtg aac gag tgc gaa act	909
Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr	
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 Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile
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 tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc 1005
 Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys
 210 215 220
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 Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu
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 Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr
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 255 260 265 270
 cac cga aac cac acg tgt acc tca ctg cag act tgc tac aat cta caa 1197
 His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln
 275 280 285
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 Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu
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 ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc 1293
 Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys
 305 310 315
 aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca 1341
 Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser

320 325 330
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 Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly
 355 360 365
 cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg 1485
 Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val
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 Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu
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<211> 423

<212> PRT

<213> Mus musculus

<400> 9

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 Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
 35 40 45
 Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
 50 55 60
 Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
 65 70 75 80
 Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu

85 90 95
 Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
 100 105 110
 Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
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 Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
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 Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
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 Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
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 Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
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 Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
 195 200 205
 Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp
 210 215 220
 Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
 225 230 235 240
 Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
 245 250 255
 Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
 260 265 270
 Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
 275 280 285
 Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu

290 295 300
 Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
 305 310 315 320
 Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
 325 330 335
 Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
 340 345 350
 Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
 355 360 365
 Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380
 Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
 385 390 395 400
 Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
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 Tyr Val Ser Gln Tyr Pro Phe
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<210> 10

<211> 1269

<212> DNA

<213> Mus musculus

<400> 10

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<211> 448

<212> PRT

<213> Homo sapiens

<400> 11

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-20

-15

-10

Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp

-5

-1 1

5

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr

10

15

20

25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly

30

35

40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr

45

50

55

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala

60

65

70

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile

75

80

85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val

90

95

100

105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys

110

115

120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp

125

130

135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr

140

145

150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys

155	160	165	
Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val			
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Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr			
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Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu			
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Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe			
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Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser			
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Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp			
250	255	260	265
Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr			
	270	275	280
Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys			
	285	290	295
Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala			
	300	305	310
Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp			
	315	320	325
Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met			
330	335	340	345
Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys			
	350	355	360
Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile			

365	370	375
Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile		
380	385	390
Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg		
395	400	405
Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe		
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<210> 12

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 12

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<210> 13

<211> 2328

<212> DNA

<213> Homo sapiens

<220>

<223> Clone human A55 derived from human brain

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<221> CDS

<222> (169).. (1512)

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<220>

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Met Pro Gly

-23

ata aaa agg ata ctc act gtt acc att ctg gct ctc tgt ctt cca agc 225

Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser

-20 -15 -10 -5

cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac ctg gat cgc 273

Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg

-1 1 5 10

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15 20 25

gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc ggg tat tta 369

Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu

30 35 40

tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac tcg aac ccc 417
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 Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu
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 Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe
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 Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys
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 Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
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 Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln
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175 180 185
 gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct 849
 Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
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 Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val
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 His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
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 His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro
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Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
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 Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
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 Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
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 Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp
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<212> PRT

<213> Homo sapiens

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Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp

290

295

300

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310

315

320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val

325

330

335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala

340

345

350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr

355

360

365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro

370

375

380

Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val

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